

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 10:42:21 ; Search time 145 seconds
(without alignments)
196.013 Million cell updates/sec

Title: US-09-622-964-6

Perfect score: 18

Sequence: 1 caggaggtccaccagcc 18

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1105431 seqs, 789497651 residues

Total number of hits satisfying chosen parameters: 242376

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
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13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
15: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	12.2	67.8	19	9	US-09-982-212-39
3	11.4	63.3	17	10	US-09-866-108-8905
4	11.4	63.3	17	10	US-09-866-108-8906
5	11.4	63.3	17	10	US-09-866-108-8907
6	11.4	63.3	17	10	US-09-866-108-8908
7	11.4	63.3	17	10	US-09-866-108-8909
8	11.4	63.3	20	9	US-09-364-609-3
9	11.2	62.2	16	9	US-09-825-805-18
10	11.2	62.2	17	9	US-09-740-332-63
11	11.2	62.2	17	9	US-09-740-332-63
12	11.2	62.2	17	10	US-09-866-108-8905
13	11.2	62.2	17	10	US-09-866-108-8906
14	11.2	62.2	17	10	US-09-866-108-8907
15	11.2	62.2	17	10	US-09-866-108-8908
16	11.2	62.2	20	9	US-10-215-112-9244
17	11.2	62.2	20	9	US-10-215-112-9245
18	11.2	62.2	20	9	US-10-215-112-9246
19	11.2	62.2	20	9	US-10-215-112-9247

c	20	11.2	62.2	20	9	US-10-215-112-9749	Sequence 9749, Ap
c	21	11.2	62.2	20	9	US-10-215-112-9750	Sequence 9750, Ap
c	22	11.2	62.2	20	9	US-10-215-112-9753	Sequence 9753, Ap
c	23	11.2	62.2	20	9	US-10-215-112-9864	Sequence 9864, Ap
c	24	11.2	62.2	20	9	US-10-215-112-9975	Sequence 9975, Ap
c	25	11.2	62.2	20	9	US-10-016-149-60	Sequence 60, Appl
c	26	11.2	62.2	20	9	US-10-016-149-61	Sequence 61, Appl
c	27	11.2	62.2	20	9	US-09-382-860-269	Sequence 269, App
c	28	10.8	60.0	15	9	US-10-010-802-217	Sequence 217, App
c	29	10.8	60.0	17	9	US-10-060-998-1110	Sequence 1110, Ap
c	30	10.8	60.0	17	9	US-10-060-998-1111	Sequence 1111, Ap
c	31	10.8	60.0	17	9	US-10-060-998-1112	Sequence 1112, Ap
c	32	10.8	60.0	17	9	US-10-060-998-1113	Sequence 1113, Ap
c	33	10.8	60.0	17	10	US-09-759-622-5	Sequence 5, Appl
c	34	10.8	60.0	17	10	US-09-866-108-7592	Sequence 7592, Ap
c	35	10.8	60.0	17	10	US-09-866-108-7593	Sequence 7593, Ap
c	36	10.8	60.0	17	10	US-09-866-108-9829	Sequence 9829, Ap
c	37	10.8	60.0	17	10	US-09-866-108-9830	Sequence 9830, Ap
c	38	10.8	60.0	17	10	US-09-866-108-9831	Sequence 9831, Ap
c	39	10.8	60.0	17	10	US-09-866-108-9832	Sequence 9832, Ap
c	40	10.8	60.0	17	10	US-09-866-607-15	Sequence 15, Appl
c	41	10.8	60.0	20	9	US-09-918-026A-58	Sequence 58, Appl
c	42	10.6	58.9	17	9	US-09-827-395A-581	Sequence 581, App
c	43	10.6	58.9	17	9	US-09-740-332-62	Sequence 62, Appl
c	44	10.6	58.9	17	10	US-09-866-108-8929	Sequence 8929, Ap
c	45	10.6	58.9	20	10	US-09-733-294A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-10-156-610-65
; Sequence 65, Application US/10156610.
; Publication No. US20030050270A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSI
; FILE REFERENCE: ISPH-0666
; CURRENT APPLICATION NUMBER: US/10/156,610
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/856,246
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US99/16959
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/197,008
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-156-610-65

Query Match 73.3%; Score 13.2; DB 9; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGAGTCCACCAGCC 18

Db 1 CAGGAGTCCACCAGCC 18

RESULT 2

US-09-982-212-39
; Sequence 39, Application US/09982212
; Publication No. US20030118998A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Frank B.

RESULT 6
US-09-866-108-8908
; Sequence 8908, Application US/09866108

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; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 8909
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8909
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Query Match 63.3%; Score 11.4; DB 10; Length 17;
Best Local Similarity 92.3%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 GAGTCCCCCAGC 17
    ||||| ||||
DB 1 GAGTCCCCCAGC 13
```

```
RESULT 8
US-09-364-609-3/c
; Sequence 3, Application US/09/364609
; Publication No. US20030036521A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Iliana
; APPLICANT: Brennen, Douglas E.
; APPLICANT: Zamostiano, Rachel
; APPLICANT: Gelber, Edgar
; APPLICANT: Pinhasov, Albert
; APPLICANT: Bassan, Merav
; APPLICANT: Ramot University Authority for Applied Research &
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Methods of Inhibiting Cancer Cells With ADNF III
; TITLE OF INVENTION: Antisense Oligonucleotides
; FILE REFERENCE: 019856-000100US
; CURRENT APPLICATION NUMBER: US/09/364,609
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antisense
; OTHER INFORMATION: oligonucleotide 9
US-09-364-609-3
```

```
Query Match 63.3%; Score 11.4; DB 9; Length 20;
Best Local Similarity 92.3%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 3 GGGAGTCCACCA 15
    |||| | |||||
DB 18 GGGAGTCCACCA 6
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RESULT 9
US-09-825-805-18/c
; Sequence 18, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucle
; FILE REFERENCE: MBH00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hepatitis C Virus
US-09-825-805-18

Query Match 62.2%; Score 11.2; DB 9; Length 16;
Best Local Similarity 81.3%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 CAGGGAGTCCACCA 16
    |||| | |||| |
DB 16 CAGGGAGTCCACCA 1
```

```
RESULT 10
US-09-740-332-63/c
; Sequence 63, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
```

; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-63

Query Match 62.2%; Score 11.2; DB 9; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCACCAG 16
||||| ||| ||||| ||
DB 16 CAGGCAGTACCACAAG 1

RESULT 11
US-09-740-332-4493
; Sequence 4493, Application US/09740332
; Publication No. US2003012570A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4493
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4493

Query Match 62.2%; Score 11.2; DB 9; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+04;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCACCAG 16
||||| ||| ||||| ||
DB 1 CAGGCAGUACCACAAG 16

RESULT 12
US-09-866-108-7594
; Sequence 7594, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-03-26

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7594
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7594

Query Match 62.2%; Score 11.2; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGGGAGTCCACCAGC 17
||||| ||| ||||| ||
DB 2 AGGAAGTCCACCATC 17

RESULT 13
US-09-866-108-7595
; Sequence 7595, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7595
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7595

Query Match 62.2%; Score 11.2; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AGGAGTCCACCAGC 17
| | | | | | | | | | | | | | | | |
Db 1 AGGAAGTCCACCAC 16

RESULT 14
US-10-005-956-860
; Sequence 860, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 860
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-860

Query Match 62.2%; Score 11.2; DB 9; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGGAGTCCACCAG 16
| | | | | | | | | | | | | | | | |
Db 3 CAGGATGCCCAACAG 18

RESULT 15
US-10-215-112-9244
; Sequence 9244, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9244
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9244

Query Match 62.2%; Score 11.2; DB 9; Length 20;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGGAGTCCACCAG 16
| | | | | | | | | | | | | | | | |
Db 5 CAGGAGGTCTACCAG 20

Search completed: July 12, 2003, 11:48:34
Job time : 147 secs

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 09:41:16 ; Search time 1867 Seconds
(without alignments)
280.584 Million cell updates/sec

Title: US-09-622-964-6
Perfect score: 18
Sequence: 1 cagggagtcaccacagcc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 332216

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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GenEmbl:*
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29: em_vi:*
30: em_hgt_hum:*
31: em_hgt_inv:*
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33: em_hgt_mus:*
34: em_hgt_pln:*
35: em_hgt_rtd:*
36: em_hgt_mam:*
37: em_hgt_vrt:*
38: em_sy:*
39: em_hgtgo_hum:*
40: em_hgtgo_mus:*
41: em_hgtgo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
C 1	12.4	68.9	20	6	AR207367 Sequence
C 2	11.8	65.6	19	6	AX129446 Sequence
C 3	11.8	65.6	19	6	AX129446 Sequence
C 4	11.4	63.3	17	6	AX132043 Sequence
C 5	11.4	63.3	17	6	AX273032 Sequence
C 6	11.4	63.3	17	6	AX273256 Sequence
C 7	11.4	63.3	17	6	AX273257 Sequence
C 8	11.4	63.3	17	6	AX474915 Sequence
C 9	11.4	63.3	17	6	AX474916 Sequence
C 10	11.4	63.3	17	6	AX474917 Sequence
C 11	11.4	63.3	17	6	AX474918 Sequence
C 12	11.4	63.3	17	6	AX474919 Sequence
C 13	11.4	63.3	19	12	AB068548 Synthetic
C 14	11.4	63.3	20	6	AX055811 Sequence
C 15	11.2	62.2	20	6	AX081461 Sequence
C 16	11.2	62.2	19	6	BD002098 Method an
C 17	11.2	62.2	19	6	BD002141 Method an
C 18	11.2	62.2	20	6	AR167047 Sequence
C 19	11	61.1	20	6	AR210702 Sequence
C 20	11	61.1	17	6	AX474920 Sequence
C 21	10.8	60.0	17	6	AX474921 Sequence
C 22	10.8	60.0	17	6	AR057480 Sequence
C 23	10.8	60.0	17	6	AR057523 Sequence
C 24	10.8	60.0	17	6	AR057564 Sequence
C 25	10.8	60.0	17	6	AR057733 Sequence
C 26	10.8	60.0	17	6	AR115238 Sequence
C 27	10.8	60.0	17	6	AR115281 Sequence
C 28	10.8	60.0	17	6	AR115322 Sequence
C 29	10.8	60.0	17	6	AR115491 Sequence
C 30	10.8	60.0	17	6	AR140637 Sequence
C 31	10.8	60.0	18	6	AX454813 Sequence
C 32	10.8	60.0	18	6	AR169781 Sequence
C 33	10.8	60.0	18	6	AR192805 Sequence
C 34	10.8	60.0	19	6	AR037229 Sequence
C 35	10.8	60.0	19	6	AR048698 Sequence
C 36	10.8	60.0	20	6	AX129445 Sequence
C 37	10.8	60.0	20	6	A04194
C 38	10.8	60.0	20	6	A04223
C 39	10.6	58.9	18	6	AX092588 Nucleotide
C 40	10.6	58.9	18	6	AR084734 Sequence
C 41	10.6	58.9	18	6	AR105376 Sequence
C 42	10.6	58.9	19	6	AX247498 Sequence
C 43	10.6	58.9	19	6	AX131323 Sequence
C 44	10.6	58.9	19	6	I84487 Sequence 11
C 45	10.6	58.9	20	6	A68403 Sequence 8
C 45	10.6	58.9	20	6	AR023735 Sequence

ALIGNMENTS

RESULT 1
AR207367/c
LOCUS AR207367 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 23 from patent US 6372889.
ACCESSION AR207367
VERSION AR207367.1 GI:21506259
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sheppard,P.O., Conklin,D.C., Farrah,T.M., Maurer,M.F. and Grossmann,A.
TITLE Soluble protein 2TMPO-1
JOURNAL Patent: US 6372889-A 23 16-APR-2002;

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source
1. .20
Location/Qualifiers
4 a 5 c 8 g 3 t
BASE COUNT
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Query Match
Best Local Similarity 68.9%; Score 12.4; DB 6; Length 20;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGTCCACACGCC 18
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Db 14 GAGTCCACACGCC 1

RESULT 2
AX129446
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/db_xref="taxon:9606"
/note="cdk6 ribozyme binding site"
3 a 9 c 3 g 4 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 65.6%; Score 11.8; DB 6; Length 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGATCCACACGCC 18
||||| |||||
Db 5 GGATCCACACGCC 19

RESULT 3
AX132043/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
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1. .19
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding site"
0 a 5 c 9 g 5 t
BASE COUNT
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Query Match
Best Local Similarity 68.9%; Score 12.4; DB 6; Length 20;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGTCCACACGCC 18
||||| |||||
Db 14 GAGTCCACACGCC 1

RESULT 2
AX129446
LOCUS
DEFINITION
ACCESSION
VERSION
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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source
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Location/Qualifiers
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/db_xref="taxon:9606"
/note="cdk6 ribozyme binding site"
3 a 9 c 3 g 4 t
BASE COUNT
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Query Match
Best Local Similarity 65.6%; Score 11.8; DB 6; Length 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGATCCACACGCC 18
||||| |||||
Db 5 GGATCCACACGCC 19

RESULT 3
AX132043/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
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FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding site"
0 a 5 c 9 g 5 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 68.9%; Score 12.4; DB 6; Length 20;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGTCCACACGCC 18
||||| |||||
Db 14 GAGTCCACACGCC 1

RESULT 2
AX129446
LOCUS
DEFINITION
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Location/Qualifiers
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/db_xref="taxon:9606"
/note="cdk6 ribozyme binding site"
3 a 9 c 3 g 4 t
BASE COUNT
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Query Match
Best Local Similarity 65.6%; Score 11.8; DB 6; Length 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGATCCACACGCC 18
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Db 5 GGATCCACACGCC 19

RESULT 3
AX132043/c
LOCUS
DEFINITION
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TITLE
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/note="Cyclin B1 ribozyme binding site"
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BASE COUNT
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Query Match
Best Local Similarity 65.6%; Score 11.8; DB 6; Length 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGATCCACACGCC 18
||||| |||||
Db 17 GGATCCACACGCC 3

RESULT 4
AX273032
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
4 a 8 c 5 g 0 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGTCCAC 13
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Db 2 CAGGAGTCCAC 14

RESULT 5
AX273256
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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1. .17
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
3 a 7 c 6 g 1 t
BASE COUNT
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Query Match
Best Local Similarity 63.3%; Score 11.4; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGTCCAC 13
||||| |||||
Db 2 CAGGAGTCCAC 14

RESULT 5
AX273256
LOCUS
DEFINITION
ACCESSION
VERSION
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
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source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
3 a 7 c 6 g 1 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGTCCAC 13
||||| |||||

Db 5 CAGGGAGGCCAC 17

RESULT 6
AX273257
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX273257
Sequence 826 from Patent WO0162911.
AX273257
AX273257.1 GI:16545994

human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and
Ellis, J.H.
Method and reagent for the inhibition of grid
Patent: WO 0162911-A 826 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

Location/Qualifiers
1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT
ORIGIN

4 a 8 c 5 g 0 t

Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 13
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Db 3 CAGGGAGGCCAC 15

RESULT 7
AX474915/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX474915
Sequence 136 from Patent WO0224750.
AX474915
AX474915.1 GI:22214200

human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Zhang, J.
Human kidney tumor overexpressed membrane protein 1
Patent: WO 0224750-A 136 28-MAR-2002;
Acomica, Inc. (US)

Location/Qualifiers
1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT
ORIGIN

3 a 6 c 5 g 3 t

Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 13
|||||

Db 17 CAGGGAGTCCCTC 5

RESULT 8
AX474916/c
LOCUS
DEFINITION
ACCESSION

AX474916
Sequence 137 from Patent WO0224750.
AX474916

human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE

Zhang, J.
Human kidney tumor overexpressed membrane protein 1

Version 1
Title Human kidney tumor overexpressed membrane protein 1
Journal Human kidney tumor overexpressed membrane protein 1
Features Location/Qualifiers
1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"

Base Count
Origin

3 a 5 c 5 g 4 t

Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 13
|||||

Db 15 CAGGGAGTCCCTC 3

RESULT 10
AX474918/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX474918
Sequence 139 from Patent WO0224750.
AX474918
AX474918.1 GI:22214203

human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE

Zhang, J.
Human kidney tumor overexpressed membrane protein 1

Version 1
Title Human kidney tumor overexpressed membrane protein 1
Journal Human kidney tumor overexpressed membrane protein 1
Features Location/Qualifiers
1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"

Base Count
Origin

3 a 5 c 5 g 4 t

Query Match 63.3%; Score 11.4; DB 6; Length 17;
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 13
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Db 15 CAGGGAGTCCCTC 3

RESULT 11
AX474919/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX474919
Sequence 138 from Patent WO0224750.
AX474919
AX474919.1 GI:22214202

human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Zhang, J.
Human kidney tumor overexpressed membrane protein 1
Patent: WO 0224750-A 138 28-MAR-2002;
Acomica, Inc. (US)

Location/Qualifiers
1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"

Base Count
Origin

3 a 5 c 5 g 4 t

Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 13
|||||

Db 16 CAGGGAGTCCCTC 4

RESULT 9
AX474917/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX474917
Sequence 137 bp DNA
AX474917
AX474917.1 GI:22214202

human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Zhang, J.
Human kidney tumor overexpressed membrane protein 1
Patent: WO 0224750-A 137 28-MAR-2002;
Acomica, Inc. (US)

Location/Qualifiers
1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"

Base Count
Origin

3 a 5 c 5 g 4 t

Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 13
|||||

Db 16 CAGGGAGTCCCTC 4

JOURNAL Patent: WO 0224750-A 139 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 3 a 4 c 6 g 4 t
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Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGGAGTCCAC 13
IIIIIIIIII
Db 14 CAGGGAGTCCCTC 2

RESULT 11
AX474919/c
LOCUS AX474919 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 140 from Patent WO0224750.
ACCESSION AX474919
VERSION AX474919.1 GI:22214204
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 140 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
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BASE COUNT 2 a 4 c 6 g 5 t
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Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGGAGTCCAC 13
IIIIIIIIII
Db 13 CAGGGAGTCCCTC 1

RESULT 12
AB068548/c
LOCUS AB068548 19 bp DNA linear SYN 08-AUG-2001
DEFINITION Synthetic construct DNA, forward primer for human STS sts-D1S2169
at 1p36.
ACCESSION AB068548
VERSION AB068548.1 GI:15129352
KEYWORDS synthetic construct DNA.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Chen, Y.Z., Hayashi, Y., Wu, J.G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
REFERENCE 2 (bases 1 to 19)
AUTHORS Horii, A.
TITLE Direct Submission

JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES Location/Qualifiers
source 1..19
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/db_xref="taxon:32630"
misc_feature 1..19
/note="forward primer for human STS sts-D1S2169 at 1p36
sts-D1S2169 obtained from clones B300M5, B92M14, B97J10,
B33P22, B69N18, B179D7, Human BAC library RPC1-11"
BASE COUNT 3 a 3 c 8 g 5 t
ORIGIN
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Best Local Similarity 92.3%; Pred. No. 7.7e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GAGTCCACACG 17
IIIIIIIIII
Db 17 GAGTCCACACG 5

RESULT 13
AX055811
LOCUS AX055811 20 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 8 from Patent WO0072885.
ACCESSION AX055811
VERSION AX055811.1 GI:12228924
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ferber, S.
TITLE Methods of inducing regulated pancreatic hormone production in non-
pancreatic islet tissues
JOURNAL Patent: WO 0072885-A 8 07-DEC-2000;
Ferber, Sarah (IL)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically synthesized"
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGGAGTCCAC 13
IIIIIIIIII
Db 8 CTGGAGTCCAC 20

RESULT 14
AX081461/c
LOCUS AX081461 20 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 3 from Patent WO0109311.
ACCESSION AX081461
VERSION AX081461.1 GI:13170283
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gozes, I., Brennen, D.E., Zamostiano, R., Gelber, E., Pinhasov, A. and
Basan, M.
TITLE Methods of inhibiting cancer cells with adnf iii antisense
oligonucleotides
JOURNAL Patent: WO 0109311-A 3 08-FEB-2001;

RAMOT UNIVERSITY (IL) : THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
(US)

FEATURES
source
Location/Qualifiers
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/db_xref="taxon:32630"
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ORIGIN /note="antisense oligonucleotide 9"

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Best Local Similarity 92.3%; Pred. No. 7.6e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GGGAGTCCACCA 15
Db 18 GGGACTCCACCA 6

RESULT 15
BD002098
LOCUS
DEFINITION Method and kit for detection of specific nucleotide sequence.
ACCESSION BD002098 19 bp DNA linear PAT 31-JAN-2002
VERSION BD002098.1 GI:18628838
KEYWORDS JP 2000189198-A/19.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ehrlich, H.A., Horne, G.T., Saiki, R.K. and Maris, C.B.
TITLE Method and kit for detection of specific nucleotide sequence
JOURNAL Patent: JP 2000189198-A 19 11-JUL-2000;
COMMENT F HOFFMANN LA ROCHE AG
OS Artificial Sequence
PN JP 2000189198-A/19
PD 11-JUL-2000
PF 24-FEB-2000 JP 2000052306
PR 13-MAR-1986 US 839331.22-AUG-1986 US 899344 PI
HENRY ANTHONY EHRLICH, GLENN THOMAS HORNE, RANDALL KEICHI SAIKI, PI
CURRY BANKS MARIS
PC C12Q1/68//C12N15/09,C12N15/00
CC
FH Key
FT source
FT Location/Qualifiers
1. .19
/organism="Artificial Sequence".

FEATURES
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGGGAGTCCACAG 16
Db 4 CAGGCAGCCACAG 19

Search completed: July 12, 2003, 11:17:36
Job time : 1871 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 09:40:21 ; Search time 226 seconds
(without alignments)
179.363 Million cell updates/sec

Title: US-09-622-964-6

Perfect score: 18

Sequence: 1 caggaggtccaccagcc 18

Scoring table: IDENTITY_NUC

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 1367302

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	20	AAZ21230
C 2	12.4	68.9	20	20	Human CGICE PCR pr
C 3	12.4	68.9	20	20	Human soluble prot
C 4	12.2	67.8	18	24	Human ZTMO-1 sequ
C 5	11.8	65.6	19	21	Human HLA genotypi
C 6	11.8	65.6	19	21	cdk6 ribozyme bind
C 7	11.8	65.6	19	22	Cyclin B1 ribozyme
C 8	11.8	65.6	19	22	cell-cycle depende
C 9	11.6	64.4	20	21	Cyclin B1 ribozyme
					Hepatitis C genome

C 10	11.4	63.3	17	24	ABQ63360
C 11	11.4	63.3	17	24	ABQ63361
C 12	11.4	63.3	17	24	ABQ63362
C 13	11.4	63.3	17	24	ABQ63363
C 14	11.4	63.3	17	24	ABQ63364
C 15	11.4	63.3	17	24	ABN08913
C 16	11.4	63.3	17	24	ABN08914
C 17	11.4	63.3	17	24	ABN08915
C 18	11.4	63.3	17	24	ABN08916
C 19	11.4	63.3	17	24	ABN08917
C 20	11.4	63.3	18	22	AAH47582
C 21	11.4	63.3	20	22	AAF34898
C 22	11.4	63.3	20	22	AAC82778
C 23	11.4	63.3	20	24	ABL45263
C 24	11.2	62.2	16	14	AAO52859
C 25	11.2	62.2	17	24	ABN07602
C 26	11.2	62.2	17	24	ABN07603
C 27	11.2	62.2	18	13	AAQ26466
C 28	11.2	62.2	19	8	AAAT71284
C 29	11.2	62.2	19	10	AAAN90050
C 30	11.2	62.2	19	12	AAQ15037
C 31	11.2	62.2	19	12	AAQ15104
C 32	11.2	62.2	20	15	AAQ44888
C 33	11.2	62.2	20	21	AAA66799
C 34	11.2	62.2	20	21	AAA37007
C 35	11.2	62.2	20	22	AAAD13533
C 36	11.1	61.1	17	24	ABQ63365
C 37	11.1	61.1	17	24	AAV08217
C 38	11.1	61.1	18	19	ABU94636
C 39	10.8	60.0	14	24	ABL94637
C 40	10.8	60.0	15	22	AAF69574
C 41	10.8	60.0	16	24	ABL94637
C 42	10.8	60.0	17	16	AAAT53533
C 43	10.8	60.0	17	16	AAAT53518
C 44	10.8	60.0	17	16	AAAT53448
C 45	10.8	60.0	17	16	AAAT53757

ALIGNMENTS

RESULT 1
AAZ21230
ID AAZ21230 standard; DNA; 18 BP.
XX
AC AAZ21230;
XX
DT 22-NOV-1999 (first entry)
XX
XX Human CGICE PCR primer SEQ ID NO:6.
DE
XX CGICE; Best's macular dystrophy; mutation; diagnosis; detection;
KW BMD; age-related macular dystrophy; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9943695-A1.
XX
PD 02-SEP-1999.
XX
PF 22-FEB-1999; 99WO-US03790.
XX
PR 25-FEB-1998; 98US-0075941.
XX
PR 18-DEC-1998; 98US-0112926.
PA (MERI) MERCK & CO INC.
PA (UYUP-) UNIV UPPSALA.
XX
PI Petrukhin K, Caskey CT, Metzker M, Wadelius C;
XX WPI; 1999-540560/45.
DR
XX

PT Human and mouse polynucleotides encoding CG1CE polypeptides -
PS Disclosure; Page 17; 67pp; English.
XX
CC The present invention describes human and mouse CG1CE polynucleotides
CC and proteins. When the CG1CE gene is mutated it is responsible for
CC Best's macular dystrophy (BMD). Polynucleotides encoding CG1CE are
CC useful for diagnosing whether a patient carries a mutation in the
CC CG1CE gene. Normal and mutated CG1CE proteins are useful for
CC identifying activators and/or inhibitors of these proteins, in order
CC to treat BMD. The CG1CE gene offers a simpler and cheaper method of
CC diagnosing BMD without the need for the presence of the patient. The
CC gene may also be useful to discovering the genetic cause of age-related
CC macular dystrophy. The present sequence represents a PCR primer for
CC the human CG1CE cDNA sequence.
XX
SQ Sequence 18 BP; 4 A; 8 C; 5 G; 1 T; 0 other;
Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGGAGTCCACCGCC 18
DB 1 CAGGGAGTCCACCGCC 18
IIIIIIIIIIIIIIIIIIII
RESULT 2
AAZ24791/c
ID AAZ24791 standard; DNA; 20 BP.
AC AAZ24791;
XX
XX
DT 31-JAN-2000 (first entry)
XX
DE Human soluble protein ZTMPO-1 DNA sequencing primer ZC16037.
XX
KW Soluble protein; ZTMPO-1; thymopoietin-emerin family; human; cancer;
KW nuclear membrane protein; cardiac disorder; autoimmune disorder; testis;
KW infectious disease; cellular proliferation; skeletal muscle; thyroid;
KW adrenal gland; tumor; spermatogenesis; sperm activation; PCR primer;
KW contraindication; immune response; humoral response; vaccination; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO954468-A1.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US08601.
XX
XX 21-APR-1998; 98US-0063838.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;
PI WPI; 1999-634003/54.
XX
XX New isolated ZTMPO-1 polypeptides used for diagnosis and treatment of
PT e.g. cancer, cardiac and autoimmune disorders and infectious diseases
PT and for developing contraceptives -
XX
XX Example 1; Page 102; 110pp; English.
PS
XX The invention provides a human soluble protein ZTMPO-1 which has
CC homology to the thymopoietin-emerin family of nuclear membrane proteins.
CC The ZTMPO-1 protein can be expressed by standard recombinant
CC methodology. Altered levels of ZTMPO-1 receptor polypeptides may be
CC indicative of pathological conditions including cancer, cardiac and
CC autoimmune disorders and infectious diseases. The nucleic acid can be
CC used as a source of hybridization probes for detecting a genetic

CC abnormality in a patient. The ZTMPO-1 polypeptides can be used to
CC modulate cellular proliferation and differentiation in a diverse array of
CC tissues such as testis, skeletal muscle, thyroid and adrenal gland.
CC Antagonists of ZTMPO-1 can be used in modulating cellular proliferation
CC and differentiation such as in tumor growth and development. They can
CC also be used for inhibiting spermatogenesis and sperm activation. Such
CC ZTMPO-1 antagonists can be used for contraception in humans and animals,
CC and in particular, domestic and zoological animals and livestock, where
CC they would act to prevent fertilization of an egg. ZTMPO-1 antagonists
CC could also be used to mediate immune response, e.g. by boosting the
CC humoral response in individuals at risk for an infectious disease or as
CC a supplement to vaccination. Sequences AAZ24777-791 represent primers
CC used for sequencing the ZTMPO-1 DNA.
XX
SQ Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 other;
Query Match 68.9%; Score 12.4; DB 20; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GAGTCCACCGCC 18
DB 14 GAGTCCACCGCC 1
IIIIIIIIIIIIIIIIIIII
RESULT 3
ABK50010/c
ID ABK50010 standard; DNA; 20 BP.
XX
AC ABK50010;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human ZTMPO-1 sequencing primer ZC16037.
XX
KW ZTMPO; human; immunosuppressive; inotropic; cardiac; leukaemia;
KW cardiant; cytostatic; antidiabetic; hypotensive; immunological; ss;
KW reproductive; muscle pathology; diabetes; muscular dystrophy;
KW haematopoietic disorder; hypertension; chromosome 12q24.33;
KW sequencing; primer; ZC16037.
XX
XX Homo sapiens.
XX
XX US6372889-B1.
XX
XX 16-APR-2002.
XX
XX 19-APR-1999; 99US-0294531.
XX
XX 21-APR-1998; 98US-082513P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;
PI WPI; 2002-350566/38.
XX
XX Novel isolated ZTMPO-1 polypeptide, useful for modulating cell
PT proliferation, and for treating disorders such as diabetes, muscular
PT dystrophy and hypertension -
XX
XX Example 1; Column 63; 40pp; English.
PS
XX This invention relates to the cDNA and protein sequences of a novel
CC isolated ZTMPO-1 polypeptide. ZTMPO-1 is a soluble protein with
CC homology to the nuclear membrane proteins emerlin and thymopoietins.
CC The protein of the invention may have immunosuppressive, inotropic,
CC cardiant, cytostatic, antidiabetic and hypotensive activities. The
CC invention also comprises antibodies to ZTMPO-1 proteins which can
CC be used to detect ZTMPO proteins and may be used to regulate the
CC function of the protein. The sequences of the invention may be used
CC for modulating cellular proliferation and differentiation, and
CC for diagnostic purposes. The polypeptides can be used to treat

CC immunological, reproductive, cardiac, and muscle pathologies, such as
 CC diabetes, muscular dystrophy, haematopoietic disorders, leukaemias, and
 CC hypertension. The present sequence represents a human ZPMO-1 gene
 CC sequencing primer used to sequence the ZPMO gene of the invention.
 XX
 XX

SO Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 other;

Query Match 68.9%; Score 12.4; DB 24; Length 20;
 Best Local Similarity 92.9%; Pred. No. 8.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGTCCACCAGCC 18
 ||||| |||||
 DB 14 GAGTCCACCAGCC 1

RESULT 4
 ABL30611/c
 ID ABL30611 standard; DNA; 18 BP.
 XX
 AC ABL30611;
 XX
 DT 21-MAR-2002 (first entry)
 XX
 DE Human HLA genotyping oligonucleotide SEQ ID NO 100.
 XX
 KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KW immunogenetic; transplantation; genetic disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192572-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-JP04662.
 XX
 PR 01-JUN-2000; 2000JP-0164798.
 XX
 PS (NLSN) NISSHINBO IND INC.
 PA (SYST-) SYSTEM RES INC.
 XX
 PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 XX
 DR WPI; 2002-122074/16.

Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes
 of individuals e.g. by determining immunogenetic differences when
 transplanting between them -
 PS Claim 10; Page 112; 345pp; Japanese.
 XX
 CC The invention relates to a typing kit for judging human leukocyte antigen
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
 CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
 CC genes e.g. belonging to HLA class I antigens on human genome and
 CC containing gene polymorphisms as alloantigens have been immobilised as
 CC primers for amplification of cleaved nucleic acids relating to gene
 CC polymorphisms. The method is useful for judging HLA genotypes of
 CC individuals by determining immunogenetic differences before transplanting
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
 CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
 CC diagnosis of genetic diseases and identifying individuals.
 XX
 SO Sequence 18 BP; 0 A; 6 C; 8 G; 4 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 18;
 Best Local Similarity 82.4%; Pred. No. 1.1e+04;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CAGGAGTCCACCAGC 17
 ||||| ||||| |||||

DB 18 CAGGAGTCCACCAGCAGC 2

RESULT 5

AAA83078
 ID AAA83078 standard; DNA; 19 BP.
 XX
 AC AAA83078;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE cdk6 ribozyme binding site #138.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KW restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28772.
 XX
 PR 04-DEC-1998; 98US-0110954.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 DR WPI; 2000-412314/35.

New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PCNA and Cyclin B1 -
 XX
 PS Disclosure; Page 56; 109pp; English.
 XX
 CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX
 SO Sequence 19 BP; 3 A; 9 C; 3 G; 4 T; 0 other;

Query Match 65.6%; Score 11.8; DB 21; Length 19;
 Best Local Similarity 86.7%; Pred. No. 1.7e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GGAGTCCACCAGCC 18
 ||||| ||||| |||||
 DB 5 GGATCCACCAGCC 19

RESULT 6

AAA85675/c
 ID AAA85675 standard; DNA; 19 BP.
 XX
 AC AAA85675;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Cyclin B1 ribozyme binding site #4.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KW restenosis; ss.
 XX
 OS Mammalia.
 XX

PN WO200032765-A2.
 XX 08-JUN-2000.
 XX 06-DEC-1999; 99WO-US28772.
 XX 04-DEC-1998; 98US-0110954.
 XX (IMMU-) IMMUSOL INC.
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX WPI; 2000-412314/35.
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 XX PCNA and Cyclin B1
 XX Disclosure; Page 96; 109pp; English.
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 XX Representative examples of ribozyme recognition sites are given in
 XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
 XX inhibiting restenosis by introduction of the ribozyme into cells.
 XX The ribozyme is resistant to endonuclease activity and hence is
 XX efficient in restenosis treatment.
 XX Sequence 19 BP; 0 A; 5 C; 9 G; 5 T; 0 other;
 SQ Query Match 65.6%; Score 11.8; DB 21; Length 19;
 Best Local Similarity 86.7%; Pred. No. 1.7e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GGAGTCCCGACCGCC 18
 DB 17 GGAGCCCGACCGCC 3
 RESULT 7
 AAH58240
 ID AAH58240 standard; DNA; 19 BP.
 XX AAH58240;
 AC AAH58240;
 DT 10-SEP-2001 (first entry)
 XX Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:664.
 DE Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 XX recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cycostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 XX 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX 26-OCT-1999; 99US-0161532.
 XX (IMMU-) IMMUSOL INC.
 PA

XX Robbins JM, Tritz R;
 PI WPI; 2001-300427/31.
 XX Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX Example 1; Page 120; 408pp; English.
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX Sequence 19 BP; 3 A; 9 C; 3 G; 4 T; 0 other;
 SQ Query Match 65.6%; Score 11.8; DB 22; Length 19;
 Best Local Similarity 86.7%; Pred. No. 1.7e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GGAGTCCCGACCGCC 18
 DB 5 GGATTCCTCCCGCC 19
 RESULT 8
 AAH60837/C
 ID AAH60837 standard; DNA; 19 BP.
 XX AAH60837;
 AC AAH60837;
 DT 10-SEP-2001 (first entry)
 XX Cyclin B1 ribozyme binding site SEQ ID NO:3261.
 DE Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 XX recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cycostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 XX 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX

PR 26-OCT-1999; 990S-0161532.
 PA (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 XX WPI; 2001-300427/31.
 DR Treating proliferative skin or eye diseases and scarring, using
 XX ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX
 XX Example 1; Page 309; 408pp; English.
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antitickling,
 CC ophthalmological, vulvar, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH5757 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 19 BP; 0 A; 5 C; 9 G; 5 T; 0 other;
 SQ
 Query Match 65.6%; Score 11.8; DB 22; Length 19;
 Best Local Similarity 86.7%; Pred. No. 1.7e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 4 GGAGTCCCGACGACC 18
 DB 17 GGAGCCCGACGACC 3
 RESULT 9
 AA288591
 ID AA288591 standard; DNA; 20 BP.
 XX
 AC AA288591;
 XX
 DT 04-MAY-2000 (first entry)
 XX
 DE Hepatitis C genome PCR primer 4.
 XX
 KW Detection; serum; plasma; probe; infection; PCR primer; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN D819832050-A1.
 XX
 XX 27-JAN-2000.
 PD
 PF 16-JUL-1998; 98DE-1032050.
 XX
 XX 16-JUL-1998; 98DE-1032050.
 PR
 PR (BIOT) BIOTEST PHARMA GMBH.
 PA
 XX Jochum C;
 XX
 XX WPI; 2000-148478/14.
 DR

XX Detection of Hepatitis C and B viral genomes in serum or plasma using
 PT specific oligonucleotide primers and probes -
 XX
 XX Claim 1c; Page 2; 7pp; German.
 XX
 CC This invention describes a novel method to detect Hepatitis C (HCV)
 CC and/or Hepatitis B (HBV) viral genomes in a serum or plasma sample using
 CC specific primers and probes. The method and oligonucleotide primers and
 CC probes are useful for the specific detection of Hepatitis C and/or
 CC Hepatitis B viral sequences in plasma and serum samples. This may be
 CC useful for preventing Hepatitis B and/or C infection in patients through
 CC contaminated blood and/or serum products. The method is able to detect
 CC all reference samples of HBV subtypes AD and AY and HCV subtypes 1 - 5
 CC with 100% accuracy. AA288588-288591 represent PCR primers used to detect
 CC HCV virus in a sample.
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 other;
 Query Match 64.4%; Score 11.6; DB 21; Length 20;
 Best Local Similarity 77.8%; Pred. No. 2.1e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 1 CAGGAGTCCCGACGACC 18
 DB 1 CAGGAGTCCCGACGACC 18
 RESULT 10
 ABQ63360/C
 ID ABQ63360 standard; DNA; 17 BP.
 XX
 AC ABQ63360;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Human KTOM1a portion (ABQ63232) probe # 73.
 XX
 KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200224750-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 21-SEP-2001; 2001WO-US29656.
 XX
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 23-MAY-2001; 2001WO-US00670.
 PR 28-AUG-2001; 2001US-0864761.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 XX Zhang J;
 XX
 XX WPI; 2002-479509/51.
 XX
 XX New human kidney tumor overexpressed membrane (KTOM1) protein and
 PT

PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in Ktomi which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone
 XX
 PS Example 2; Page 167; 418pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid encoding human
 CC Ktomi (kidney tumour overexpressed membrane) protein. The protein of the
 CC invention has cytotatic activity. The nucleotide may have a use in gene
 CC therapy. The Ktomi nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human Ktomi.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in Ktomi which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human Ktomi (ABQ63322).
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 other;

Query Match 63.3%; Score 11.4; DB 24; Length 17;
 Best Local Similarity 92.3%; Pred. No. 2.6e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGGGAGTCCAC 13
 |||||
 Db 17 CAGGGAGTCCCTC 5

RESULT 11
 ABQ63361/c
 ID ABQ63361 standard; DNA; 17 BP.
 XX
 AC ABQ63361;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Human Ktomi portion (ABQ63322) probe # 74.
 XX
 KW Human; Ktomi; Ktomi; kidney tumour overexpressed membrane; cytotatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200224750-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 21-SEP-2001; 2001WO-US29656.
 XX
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 23-MAY-2001; 2001US-0864761.
 PR 28-AUG-2001; 2001US-315676P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhang J;
 XX
 DR WPI; 2002-479509/51.
 XX

PT New human kidney tumor overexpressed membrane (Ktomi) protein and
 PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in Ktomi which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone
 XX
 PS Example 2; Page 167; 418pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid encoding human
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 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in Ktomi which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human Ktomi (ABQ63322).
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 other;

Query Match 63.3%; Score 11.4; DB 24; Length 17;
 Best Local Similarity 92.3%; Pred. No. 2.6e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGGGAGTCCAC 13
 |||||
 Db 16 CAGGGAGTCCCTC 4

RESULT 12
 ABQ63362/c
 ID ABQ63362 standard; DNA; 17 BP.
 XX
 AC ABQ63362;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Human Ktomi portion (ABQ63322) probe # 75.
 XX
 KW Human; Ktomi; Ktomi; kidney tumour overexpressed membrane; cytotatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200224750-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 21-SEP-2001; 2001WO-US29656.
 XX
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 23-MAY-2001; 2001US-0864761.
 PR 28-AUG-2001; 2001US-315676P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhang J;
 XX
 DR WPI; 2002-479509/51.
 XX

XX New human kidney tumor overexpressed membrane (KTOM1) protein and
 PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone -
 XX Example 2; Page 167; 418pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding human
 CC KTOM1 (kidney tumor overexpressed membrane) protein. The protein of the
 CC invention has cytostatic activity. The nucleotide may have a use in gene
 CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human KTOM1.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in KTOM1 which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human KTOM1a (AB063232).
 XX Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 other;

Query Match 63.3%; Score 11.4; DB 24; Length 17;
 Best Local Similarity 92.3%; Pred. No. 2.6e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGGGAGTCCAC 13
 Db 15 CAGGGAGTCCCTC 3

RESULT 13
 AB063363/c
 ID AB063363 standard; DNA; 17 BP.

XX AC AB063363;
 XX 20-AUG-2002 (first entry)
 XX Human KTOM1a portion (AB063232) probe # 76.
 XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 OS Homo sapiens.
 XX WO200224750-A2.
 XX 28-MAR-2002.

XX 21-SEP-2001; 2001WO-US29656.
 XX 21-SEP-2000; 2000US-234687P.
 XX 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 23-MAY-2001; 2001US-0864761.
 PR 28-AUG-2001; 2001US-315676P.

(AEOM-) AEOMICA INC.

Zhang J;

XX

DR WPI; 2002-479509/51.
 XX New human kidney tumor overexpressed membrane (KTOM1) protein and
 PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone -
 XX Example 2; Page 167; 418pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding human
 CC KTOM1 (kidney tumor overexpressed membrane) protein. The protein of the
 CC invention has cytostatic activity. The nucleotide may have a use in gene
 CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human KTOM1.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in KTOM1 which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human KTOM1a (AB063232).
 XX Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 other;

Query Match 63.3%; Score 11.4; DB 24; Length 17;
 Best Local Similarity 92.3%; Pred. No. 2.6e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGGGAGTCCAC 13
 Db 14 CAGGGAGTCCCTC 2

RESULT 14
 AB063364/c
 ID AB063364 standard; DNA; 17 BP.

XX AC AB063364;
 XX 20-AUG-2002 (first entry)
 XX Human KTOM1a portion (AB063232) probe # 77.
 XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 OS Homo sapiens.
 XX WO200224750-A2.
 XX 28-MAR-2002.

XX 21-SEP-2001; 2001WO-US29656.
 XX 21-SEP-2000; 2000US-234687P.
 XX 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 23-MAY-2001; 2001US-0864761.
 PR 28-AUG-2001; 2001US-315676P.

(AEOM-) AEOMICA INC.

Zhang J;

PI

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 10:26:01 ; Search time 1624 Seconds
(without alignments)
179.507 Million cell updates/sec

Title: us-09-622-964-6

Perfect score: 18

Sequence: 1 caggaggtccaccagcc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 5800

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_othr:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10.4	57.8	19	9	AI056541
C 2	9.2	51.1	20	17	AZ848532
C 3	9	50.0	20	13	BM392896
C 4	9	50.0	20	13	BM394288
5	8.8	48.9	19	17	AZ351194
6	8.8	48.9	19	17	AZ788326

C 7	8.8	48.9	20	13	BM399755
C 8	8.6	47.8	19	17	AZ651069
C 9	8.6	47.8	20	17	AZ331568
10	8.4	46.7	19	10	AM063940
C 11	8.4	46.7	19	17	AZ323681
C 12	8.4	46.7	19	17	AZ411255
C 13	8.4	46.7	19	17	AZ775541
C 14	8.4	46.7	20	17	AZ773525
C 15	8.2	45.6	16	9	AI248882
C 16	8.2	45.6	19	17	AZ477353
C 17	8.2	45.6	19	17	AZ990851
C 18	8.2	45.6	20	13	BM395053
C 19	8	44.4	19	9	AI252235
C 20	8	44.4	19	17	AZ314143
C 21	8	44.4	19	17	AZ646713
C 22	8	44.4	20	17	AQ074235
C 23	8	44.4	20	17	AZ309592
C 24	8	44.4	20	17	AZ436106
C 25	8	44.4	20	17	AZ445379
C 26	8	44.4	20	17	AZ823352
C 27	8	44.4	20	17	AZ862319
C 28	7.8	43.3	18	14	BQ790001
C 29	7.8	43.3	18	17	AQ026356
C 30	7.8	43.3	19	17	AZ486389
C 31	7.8	43.3	19	17	AZ656937
C 32	7.8	43.3	20	9	AU254255
C 33	7.8	43.3	20	14	D18243
C 34	7.8	43.3	20	17	AZ309156
C 35	7.8	43.3	20	17	AZ478502
C 36	7.8	43.3	20	17	AZ490187
C 37	7.8	43.3	20	17	AZ835099
C 38	7.6	42.2	19	9	AI049374
C 39	7.6	42.2	19	17	AZ837373
C 40	7.6	42.2	20	17	AZ468517
C 41	7.4	41.1	16	9	AI590540
C 42	7.4	41.1	19	9	AA909236
C 43	7.4	41.1	19	9	AA928040
C 44	7.4	41.1	19	9	AI641650
C 45	7.4	41.1	19	9	AI758301

ALIGNMENTS

RESULT 1

AI056541/c

LOCUS

DEFINITION

AI056541

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI056541
cy98c11.x1 Soares fetal_liver_spleen linear EST 29-SEP-1998
clone IMAGE:1673876 3' similar to TR:014731 014731
MEMBRANE-ASSOCIATED KINASE. [1] ; mRNA sequence.

AI056541

AI056541.1 GI:3330407

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 19)

NCI-CCGAP http://www.ncbi.nlm.nih.gov/ccgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: ccgaps-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 702 Std Error: 0.00

Seq Primer: -40m3 fwd. Et from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Homo sapiens"

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 0 a 5 c 14 g 1 t
ORIGIN

Query Match 51.1%; Score 9.2; DB 17; Length 20;
Best Local Similarity 78.6%; Pred. No. 2e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCAC 14
||||| |||||
Db 15 CAGGGGGCCCCC 2

RESULT 3
BM392896/c
LOCUS
DEFINITION
BM392896 20 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM392896.1 GI:18192949
Tetrahymena thermophila.
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..20
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (small fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 3 a 7 c 7 g 3 t
ORIGIN

Query Match 50.0%; Score 9; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAGTCCCA 12
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Db 11 GGAGTCCCA 3

/db_xref="taxon:9606"
/clone_image="1673876"
/clone_lib="Soares_fetal_liver_spleen_infls_sl"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5',
AACTGGAAGATTAATTAAAGATCTTTTGTGTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 1 a 5 c 10 g 3 t
ORIGIN

Query Match 57.8%; Score 10.4; DB 9; Length 19;
Best Local Similarity 91.7%; Pred. No. 5.6e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTCCACACGACC 18
|||||||
Db 16 GGCCACACGACC 5

RESULT 2
AZ848532/c
LOCUS
DEFINITION
AZ848532 20 bp DNA linear GSS 21-FEB-2001
Clone UUGC2M0149M01 R, DNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ848532.1 GI:13031714
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0149 row: M column: 01
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0149M01"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

BASE COUNT 1 a 5 c 10 g 3 t
ORIGIN

Query Match 50.0%; Score 9; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAGTCCCA 12
|||||||
Db 11 GGAGTCCCA 3

BASE COUNT 3 a 7 c 7 g 3 t
ORIGIN

Query Match 50.0%; Score 9; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAGTCCCA 12
|||||||
Db 11 GGAGTCCCA 3

RESULT 4
BM394288/c
LOCUS
DEFINITION
50072-2-3-A03.f.1 Chilcoat/Turkewitz CDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM394288
VERSION
BM394288.1 GI:18194341
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..20

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz CDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

3 a 7 g 3 t

BASE COUNT
ORIGIN
Query Match 50.0%; Score 9; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGAGTCCA 12

|||||||

Db 11 GGAGTCCA 3

RESULT 5
A2351194
LOCUS
DEFINITION
A2351194
ACCESSION
A2351194
VERSION
A2351194.1 GI:10430431
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
house musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: A column: 08

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_lib="UUGC1M0089A08"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pWD42n; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was ligated

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 1 g 4 t

ORIGIN

Query Match 48.9%; Score 8.8; DB 17; Length 19;

Best Local Similarity 83.3%; Pred. No. 3.1e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTCCACCAGC 17

|||||||

Db 4 AATCCACCAC 15

RESULT 6

A2788326

LOCUS

DEFINITION

2M0035P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0035P16 F, DNA sequence.

ACCESSION

A2788326

VERSION

A2788326.1 GI:12928014

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: P column: 16
Seq primer: CTTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0035P16"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1147321141qb1AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      7 a      6 c      3 g      3 t
ORIGIN
Query Match      48.9%; Score 8.8; DB 17; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.1e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 AGTCCACACG 17
        | | | | | | | |
DB      1 ATTCCACCAAC 12

RESULT 7
BM399755/c
LOCUS      BM399755      20 bp mRNA linear EST 17-JAN-2002
DEFINITION      5009-0-60-H10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
                Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM399755
VERSION        BM399755.1 GI:18199808
KEYWORDS
SOURCE
ORGANISM      Tetrahymena thermophila.
                Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
                Hymenostomatida; Tetrahymenina; Tetrahymena.
                1 (bases 1 to 20)
                Turkewitz A.P., Karter, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
                J. and Klobutcher, L.
                EST from Tetrahymena thermophila, strain CU428.1, growing cells
                Unpublished (2002)
                Contact: Turkewitz AP
                Molecular Genetics and Cell Biology
                University of Chicago
                920 E. 58th Street, Chicago, IL 60637, USA
                Tel: 773 702 4374
                Fax: 773 702 3172
                Email: apturkew@midway.uchicago.edu
                Seq primer: T3.

```

```

Location/Qualifiers
1. .20
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      1 a      6 c      10 g      3 t
ORIGIN
Query Match      48.9%; Score 8.8; DB 13; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.1e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGGAGTCCAC 14
        | | | | | | | |
DB      12 GGGAGTCCAC 1

RESULT 8
AZ651069/c
LOCUS      AZ651069      19 bp DNA linear GSS 14-DEC-2000
DEFINITION      1M0521L06R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
                clone UUCG1M0521L06 R, DNA sequence.
ACCESSION      AZ651069
VERSION        AZ651069.1 GI:11786190
KEYWORDS      GSS.
SOURCE        house mouse.
ORGANISM      Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 19)
                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
                Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
                M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                and Wright, D., Weiss, R.
                Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
                Unpublished (2000)
                Contact: Robert B. Weiss
                University of Utah Genome Center
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0521 row: L column: 06
                Seq primer: CACACAGGAACAGCATGACG
                Class: plasmid ends
                High quality sequence stop: 19.
                Location/Qualifiers
                1. .19
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUCG1M0521L06"
                /clone_lib="Mouse 10kb plasmid UUCG1M library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gii14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match 47.8%; Score 8.6; DB 17; Length 19;
Best Local Similarity 73.3%; Pred. No. 3.8e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGAGGTCACACGAC 17
Db 15 GGGGGTCCCAAGAC 1

RESULT 9
A2331568
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

IM0059N03R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0059N03 R, DNA sequence.
A2331568
A2331568.1 GI:10394387
GSS
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: N column: 03

Seq primer: CACACAGGACACGATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES
source
Location/Qualifiers
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0059N03"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMDA2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gii14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match 47.8%; Score 8.6; DB 17; Length 20;
Best Local Similarity 73.3%; Pred. No. 3.9e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GGAGTCCACACGCC 18
Db 2 GCAGTCCCACTAAC 16

RESULT 10
AW063940
LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DP0975 KRIBB Human DP Intrathymic T-cell cDNA library Homo sapiens CDNA 3', mRNA sequence.
AW063940
AW063940.1 GI:8887877
EST.
human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 19)

REFERENCE

AUTHORS

Goh, S.-H., Park, J.-H., Lee, Y.-J., Lee, H.-S., Lee, I.-C.,

Park, J.-H., Kim, Y.-S. and Lee, C.-C.

Gene expression profile and identification of differentially

expressed transcripts during human intrathymic T-cell development

by cDNA sequencing analysis

Genomics 70 (1), 1-18 (2000)

20541704

COMMENT

Contact: Sung-Ho Goh

Genome Center

Korea Research Institute of Bioscience and Biotechnology

Oun-dong 52, Yu Sung-Gu, Daejeon 305-333, Republic of Korea

Tel: 82-42-860-4473

Fax: 82-42-860-4479

Email: gohsh@mail.kribb.re.kr

Seq primer: T7

High quality sequence stop: 15

POLYA=No.

FEATURES

source

Location/Qualifiers

1..19

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="KRIBB Human DP Intrathymic T-cell cDNA library"

/tissue_type="Thymus"

/cell_type="Intrathymic T-cell"

/dev_stage="CD3+4+8+ double positive stage"

/note="Vector: pGEM-T; cDNA was made from total cytoplasmic RNA of sorted human intrathymic CD3+4+8+ T-cell, adaptor ligated, amplified with PCR, and cloned into pGEM-T vector."

8 a

7 c

3 g

1 t

BASE COUNT

ORIGIN

Query Match 46.7%; Score 8.4; DB 10; Length 19;
Best Local Similarity 90.0%; Pred. No. 4.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CCACACGACGCC 18
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Db          1  CCCACGAGTC 10

RESULT 11
AZ323681/c
LOCUS
DEFINITION
  19 bp      DNA      linear      GSS 29-SEP-2000
  clone UUGC1M0045E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0045E13 F, DNA sequence.
ACCESSION
AZ323681
VERSION
AZ323681.1  GI:10378640
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: F column: 13
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
Location/Qualifiers
1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0045E13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      2 a      5 c      8 g      4 t
ORIGIN
Query Match      46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 4.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db          18  CCCACGGGCC 9

RESULT 12
AZ411255/c
LOCUS
DEFINITION
  19 bp      DNA      linear      GSS 03-OCT-2000
  clone UUGC1M0184C18 F, DNA sequence.
ACCESSION
AZ411255
VERSION
AZ411255.1  GI:10535268
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0184 row: C column: 18
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
Location/Qualifiers
1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0184C18"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      7 a      4 c      4 g      4 t
ORIGIN
Query Match      46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 4.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          6  AGTCCACACA 15
      ||||| |||||

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Db          10 ACTCACCA 1
RESULT 13
A2775541/c
LOCUS
DEFINITION
  2M0008H17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0008H17 F, DNA sequence.
ACCESSION
A2775541
VERSION
A2775541.1 GI:12902185
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
TITLE
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COMMENT
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: H column: 17
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
Location/Qualifiers
1..19
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0008H17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT
0 a 2 c 14 g 3 t
ORIGIN
Query Match
Best Local Similarity 46.7%; Score 8.4; DB 17; Length 19;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CAGGAGTCCACGACC 18
|| ||| ||| ||| |||

Db          18 CACAGAGCCCCCCCCC 1
RESULT 14
A2773525/c
LOCUS
DEFINITION
  2M0001B04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0001B04 F, DNA sequence.
ACCESSION
A2773525
VERSION
A2773525.1 GI:12897980
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
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Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0001 row: B column: 04
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0001B04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT
2 a 4 c 7 g 7 t
ORIGIN
Query Match
Best Local Similarity 46.7%; Score 8.4; DB 17; Length 20;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 TCCACGACC 17
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Db          15 TCACACCAGC 6

RESULT 15
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LOCUS
DEFINITION
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qu73e07.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:1977732 3',
similar to SW:CAL3_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN. ;,
mRNA sequence.
ACCESSION
AI248882
VERSION
AI248882.1 GI:3844279
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 16)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute / National Institute of Neurological
TITLE
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
JOURNAL
Unpublished (1998)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
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Trace considered overall poor quality
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.
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Location/Qualifiers
1..16
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/tissue_type="tumor, 5 pooled (see description)"
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/note="Organ: brain; Vector: pCMV-SPORT6; Site:1; SalI;
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
BASE COUNT      2 a      10 c      4 g      0 t
ORIGIN

Query Match      45.6%; Score 8.2; DB 9; Length 16;
Best Local Similarity 76.9%; Pred. No. 5.7e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 AGTCCACACGCG 18
      |||||||
Db      1 AGGCCCCACCGCG 13.

Search completed: July 12, 2003, 11:44:57
Job time : 1631 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 10:39:36 ; Search time 47 Seconds
(without alignments)
117.451 Million cell updates/sec

Title: US-09-622-964-6

Perfect score: 18

Sequence: 1 caggaggtccaccagcc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 247290

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/lna/5A-COMB.seq.*
- 2: /cgn2_6/ptodata/1/lna/5B-COMB.seq.*
- 3: /cgn2_6/ptodata/1/lna/6A-COMB.seq.*
- 4: /cgn2_6/ptodata/1/lna/6B-COMB.seq.*
- 5: /cgn2_6/ptodata/1/lna/PCTUS-COMB.seq.*
- 6: /cgn2_6/ptodata/1/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	12.4	68.9	20	4	US-09-294-531B-23
2	11.4	63.3	18	4	US-09-630-706-61
3	11.2	62.2	20	4	US-08-397-220B-64
4	11.2	62.2	20	4	US-08-650-093C-64
5	11.2	62.2	20	4	US-09-270-391-10
6	10.8	60.0	17	2	US-08-292-620A-1684
7	10.8	60.0	17	2	US-08-292-620A-1727
8	10.8	60.0	17	2	US-08-292-620A-1768
9	10.8	60.0	17	2	US-08-292-620A-1937
10	10.8	60.0	17	2	US-08-292-620A-1727
11	10.8	60.0	17	3	US-09-071-845-1684
12	10.8	60.0	17	3	US-09-071-845-1727
13	10.8	60.0	17	3	US-09-071-845-1768
14	10.8	60.0	17	3	US-09-071-845-1937
15	10.8	60.0	17	4	US-09-040-774-5
16	10.8	60.0	18	3	US-09-189-760-4
17	10.8	60.0	18	3	US-09-188-811-4
18	10.8	60.0	18	4	US-09-514-422-4
19	10.8	60.0	19	1	US-08-584-040-8293
20	10.8	60.0	19	1	US-08-399-986B-19
21	10.8	60.0	20	1	US-08-493-754A-19
22	10.8	60.0	20	1	US-07-841-652-26
23	10.8	60.0	20	1	US-08-446-530-2
24	10.8	60.0	20	1	US-08-446-530-4
25	10.8	60.0	20	2	US-09-097-562-2
26	10.8	60.0	20	2	US-09-097-562-4
27	10.6	58.9	18	2	US-08-691-814B-58
c 27	10.6	58.9	18	3	US-09-197-380-14

c 28	10.6	58.9	18	4	US-09-387-044B-21
29	10.6	58.9	19	1	US-08-460-853-11
30	10.6	58.9	19	4	US-09-312-748-10
c 31	10.6	58.9	20	1	US-08-782-047-17
c 32	10.6	58.9	20	3	US-09-280-799-194
c 33	10.6	58.9	20	3	US-08-924-870A-17
34	10.4	57.8	15	1	US-08-363-240A-107
35	10.4	57.8	15	1	US-08-363-240A-636
36	10.4	57.8	15	1	US-08-584-040-7977
c 37	10.4	57.8	17	4	US-08-671-947-13
c 38	10.4	57.8	18	1	US-08-671-947-14
39	10.4	57.8	18	1	US-08-250-858A-31
c 40	10.4	57.8	20	2	US-08-756-806A-31
c 41	10.4	57.8	20	3	US-09-143-214-31
c 42	10.4	57.8	20	3	US-09-000-136-17
c 43	10.4	57.8	20	4	US-09-593-589-82
c 44	10.4	57.8	20	4	US-09-506-073-33
c 45	10.4	57.8	20	4	US-09-506-073-33

ALIGNMENTS

RESULT 1

US-09-294-531B-23/C
; Sequence 23, Application US/09294531B
; Patent No. 6372889
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Farrah, Theresa M.
; APPLICANT: Mauer, Mark F.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: SOLUBLE PROTEIN ZTPPO-1
; FILE REFERENCE: 97-67
; CURRENT APPLICATION NUMBER: US/09/294,531B
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/082,513
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide 16037
US-09-294-531B-23

Query Match
Best Local Similarity 68.9%; Score 12.4; DB 4; Length 20;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGTCCCAACAGCC 18
DB 14 GAGTCCCAACAGCC 1

RESULT 2

US-09-630-706-61
; Sequence 61, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RTS-0053
; CURRENT APPLICATION NUMBER: US/09/630,706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 61
; LENGTH: 18
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-630-706-61

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Best Local Similarity 92.3%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTCCACGAGCC 18
Db      2 AGTCCACGAGCC 14

RESULT 3
US-08-397-220B-64
; Sequence 64, Application US/08397220B
; Patent No. 6284458
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment
; OF Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,220B
; FILING DATE: 09-Mar-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/01293
; FILING DATE: 10-Sep-93
; APPLICATION NUMBER: JP 5-87195
; FILING DATE: 14-Apr-93
; APPLICATION NUMBER: 07/945,289
; FILING DATE: 10-Sep-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-397-220B-64

Query Match      62.2%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CAGGGAGTCCACGAG 16
Db      5 CAGGCAGTACCACAG 20

RESULT 4
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US-08-650-093C-64
; Sequence 64, Application US/08650093C
; Patent No. 6391542
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment Of
; Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LICATA & TYRRELL P.C.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,093C
; FILING DATE: 17-May-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/452,841
; FILING DATE: May 30, 1995
; APPLICATION NUMBER: 08/397,220
; FILING DATE: March 9, 1995
; APPLICATION NUMBER: 07/945,289
; FILING DATE: September 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-650-093C-64

Query Match      62.2%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CAGGGAGTCCACGAG 16
Db      5 CAGGCAGTACCACAG 20

RESULT 5
US-09-270-391-10/C
; Sequence 10, Application US/09270391A
; Patent No. 6410233
; GENERAL INFORMATION:
; APPLICANT: de Belle, Ian
; APPLICANT: Adamson, Eileen
; APPLICANT: Marcola, Dan
; TITLE OF INVENTION: Isolation and Identification of Control Sequences and
; Factors Modulating Genes Modulated by Transcription Factors
; FILE REFERENCE: PS-00101.P.1
; CURRENT APPLICATION NUMBER: US/09/270,391A
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
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; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-270-391-10

Query Match 62.2%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 3 GGGAGTCCACCAGC 18

Db 17 GGGGTCCCTCAGCC 2

RESULT 6

US-08-292-620A-1684
; Sequence 1684, Application US/08292620A
; Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1684:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-292-620A-1684

Query Match

Best Local Similarity 60.0%; Score 10.8; DB 2; Length 17;

Matches 11; Conservative 0; Mismatches 2; Indels 3; Gaps 0;

Matches 11; Conservative 1; Mismatches 2; Indels 3; Gaps 0;

QY 3 GGGAGTCCACCAG 16

Db 1 GGGAGUACACCAG 14

RESULT 7

US-08-292-620A-1727
; Sequence 1727, Application US/08292620A
; Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1727:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-292-620A-1727

Query Match

Best Local Similarity 60.0%; Score 10.8; DB 2; Length 17;

Matches 11; Conservative 1; Mismatches 2; Indels 3; Gaps 0;

QY 3 GGGAGTCCACCAG 16

Db 3 GGGAGUACACCAG 16

RESULT 8

US-08-292-620A-1768
; Sequence 1768, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292.620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008.895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989.849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1768:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1768

Query Match 60.0%; Score 10.8; DB 2; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGTCCACCAG 16

Db 1 GGGAGUACACCAG 14

RESULT 9

US-08-292-620A-1937
; Sequence 1937, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292.620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008.895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989.849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1937:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1937

Query Match 60.0%; Score 10.8; DB 2; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGTCCACCAG 16

Db 3 GGGAGUACACCAG 16

RESULT 10

US-09-071-845-1684
; Sequence 1684, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION

;; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
;; NUMBER OF SEQUENCES: 2390
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; COUNTRY: California
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/071,845
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/292,620
;; FILING DATE: August 17, 1994
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 208/149
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;;
;; INFORMATION FOR SEQ ID NO: 1684:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-09-071-845-1684

Query Match 60.0%; Score 10.8; DB 3; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGGAGTCCACCAG 16
Db 1 GGGAGUACACCAG 14

RESULT 11

US-09-071-845-1727
; Sequence 1727, Application US/09071845
; Patent No. 6132967

GENERAL INFORMATION:

;; APPLICANT: Susan Grimm
;; APPLICANT: Dan T. Stinchcomb
;; APPLICANT: James McSwigen
;; APPLICANT: Sean Sullivan
;; APPLICANT: Kenneth G. Draper
;; TITLE OF INVENTION: RIBOZYME TREATMENT OF
;; TITLE OF INVENTION: DISEASES OR CONDITIONS
;; TITLE OF INVENTION: RELATED TO LEVELS OF
;; TITLE OF INVENTION: INTRACELLULAR ADHESION
;; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
;; NUMBER OF SEQUENCES: 2390
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles

;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/071,845
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/292,620
;; FILING DATE: August 17, 1994
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 208/149
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;;
;; INFORMATION FOR SEQ ID NO: 1727:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-09-071-845-1727

Query Match 60.0%; Score 10.8; DB 3; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGGAGTCCACCAG 16
Db 3 GGGAGUACACCAG 16

RESULT 12

US-09-071-845-1768
; Sequence 1768, Application US/09071845
; Patent No. 6132967

GENERAL INFORMATION:

;; APPLICANT: Susan Grimm
;; APPLICANT: Dan T. Stinchcomb
;; APPLICANT: James McSwigen
;; APPLICANT: Sean Sullivan
;; APPLICANT: Kenneth G. Draper
;; TITLE OF INVENTION: RIBOZYME TREATMENT OF
;; TITLE OF INVENTION: DISEASES OR CONDITIONS
;; TITLE OF INVENTION: RELATED TO LEVELS OF
;; TITLE OF INVENTION: INTRACELLULAR ADHESION
;; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
;; NUMBER OF SEQUENCES: 2390
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; COUNTRY: California
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292.620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008.895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989.849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1768:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1768

Query Match 60.0%; Score 10.8; DB 3; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGTCCACCAG 16
|||||: |||||
Db 1 GGGAGUAUCCAG 14

RESULT 13
US-09-071-845-1937
Sequence 1937, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
NUMBER OF SEQUENCES: MOLECULE-1 (1-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/292.620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008.895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989.849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1937:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1937

Query Match 60.0%; Score 10.8; DB 3; Length 17;
Best Local Similarity 78.6%; Pred. No. 5.8e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGTCCACCAG 16
|||||: |||||
Db 3 GGGAGUAUCCAG 16

RESULT 14
US-09-040-774-5
Sequence 5, Application US/09040774
Patent No. 6207811
GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Kestila, Marjo
APPLICANT: Lenkkeri, Ulla
APPLICANT: Mannikko, Minna
TITLE OF INVENTION: Nephlin Gene and Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive, Suite 3200
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040.774
FILING DATE: 18 MAR 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 97,842
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer intron 23"

US-09-040-774-5

Query Match 60.0%; Score 10.8; DB 4; Length 17;
 Best Local Similarity 85.7%; Pred. No. 5.8e+03;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGGGAGTCCACC 14
 | | | | | | | | | |
 Db 3 CGGGGAGACCCACC 16

RESULT 15

US-09-189-760-4
 ; Sequence 4, Application US/09189760
 ; Patent No. 6031078
 ; GENERAL INFORMATION:
 ; APPLICANT: Khodadoust, Mehran
 ; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
 ; FILE OF INVENTION: THEREFOR
 ; FILE REFERENCE: MNI-046CP2
 ; CURRENT APPLICATION NUMBER: US/09/189,760
 ; EARLIER APPLICATION NUMBER: 1998-11-10
 ; EARLIER FILING DATE: 1998-11-10
 ; EARLIER FILING DATE: 1998-09-29
 ; EARLIER APPLICATION NUMBER: 60/089,467
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: (PENDING)
 ; EARLIER FILING DATE: 1998-11-09
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-189-760-4

Query Match 60.0%; Score 10.8; DB 3; Length 18;
 Best Local Similarity 85.7%; Pred. No. 5.8e+03;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GAGTCCACCCAGCC 18
 | | | | | | | | | |
 Db 5 GAGTCCACTGGCC 18

Search completed: July 12, 2003, 11:45:54
 Job time : 49 secs